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☐ 1: XM_171629. Homo sapiens simi...[gi:22062231]

Links

LOCUS LOC257238 1295 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens similar to cortical granule serine protease 1

precursor (LOC257238), mRNA.

ACCESSION XM_171629

VERSION XM_171629.1 GI:22062231

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1295)

AUTHORS NCBI Annotation Project.

TITLE

Direct Submission

JOURNAL Submitted (31-JUL-2002) National Center for Biotechnology

Information, NIH, Bethesda, MD 20894, USA

COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was

predicted from NCBI contig NT_009782 by automated computational

analysis using gene prediction method: GenomeScan, supported by EST

evidence. Also see:

Documentation of NCBI's Annotation Process

FEATURES Location/Qualifiers

scurce 1..1295

organism="Homo sapiens"

hb_xref="taxon:9606"

chromosome="17"

gener 1...1295

gene "LOC257238"

/db_xre:="InterimID:257258"

cps 168..1295

/gene="L0C257238"

/rodon_start=1

product="similar to cortical granule serine protease 1

precursor"

protein id="XP 101629.1"

TO MARTINE AND REPORT OF THE PROPERTY OF THE P

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note="Region: smart(00020, Tryp_SPc, Trypsin-like serine")
                     protease; Many of these are synthesised as inactive
                     precursor hymogens that are cleaved during limited
                     proteolysis to generate their active forms. A few,
                     however, are active as single chair molecules, and others
                     are inactive due to substitutions of the catalytic triad
                     residues"
     misc feature
                     :71..434
                     gene="L00257238"
                     note="Region: pfam00089, trypsin, Trypsin"
     misc feature
                     819..1199
                     gene="L00257238"
                     .note="Region: pfam02395, IGA1, Immunoglobulin A1
                     protease. This family consists of immunoglobulin Al
                     protease proteins. The immunoglobulin Al protease cleaves
                     immunoglobulin IgA and is found in pathogenic bacteria
                     such as Neisseria gonorrhoeae Not all of the members of
                     this family are IgA proteases (one member from E. coli
                     cleaves human coagulation factor V, another one is a
                     hemoglobin protease) "
     misc feature
                     900..1187
                     gene="L00257238"
                     note="Fegion: smart00020, Tryp_SPc, Trypsin-like serine
                     protease; Many of these are synthesised as inactive
                     precursor symogens that are cleaved during limited
                     proteolysis to generate their active forms. A few,
                     however, are active as single chain molecules, and others
                     are inactive due to substitutions of the catalytic triad
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BASE COUNT
                352 a
                         265 c 314 a 364 t
ORIGIN
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       61 aagdadaago iggogdatgo oogigggigg igaqootgda qaitaaatat goodgigtid
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      181 tgattggaac taataatata catggacget atesteatas caagaagata aaaattaaag
      241 caatcattat teatecaaac tteattttgg aatettatgt aaatgatatt geacttttte
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     361 ttttccaaat cotggacgga aacacaaagt gttttataag tggctgggga agaacaaaag
     421 aagaaggtat agcaggetit gtgactgtgg tgtcctgtgg tetttacaag ctaaagtaca
      481 qaaqaqatea qaaaatgtea attsatetta ticacatqaq aqiiqotgee caaqqattio
      541 trattagado tabametata detradadet tidadadada egeacetgeg atageettae
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The control of the co

[&]quot;我们们是我们的,我们的我们的,我们就是我们的,我们就是我们的,我们就是这个人,我们就会看到这样。"

1261 ctttatgttt tgtcatctta ctagcaacaa cataa

Revised: July 5, 2002.

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 $\{x_{i,k} \in \mathbb{N} \mid i \leq i \leq a \leq a\}$

Identities = 141/153 (92%), Positives = 141/153 (92%) Frame = +3

Query: 62 CGTAPLKDVLQGSFIIGGTEAQAGAWPWVVSLQIKYGRVLVHVCGGTLVRERWVLTAAHC 121 CGTAPLKDVLQGSFIIGGTEAQAGAWPWVVSLQIKYGEVLVHVCGGTLVRE

Sbjct: 3 CGTAPLKDVLQGSFIIGGTEAQAGAWPWVVSLQIKYGEVLVHVCGGTLVRE------ 155

Query: 122 TKDSDPLMWTAVIGTNNIHGRYPHTKKIKIKAIIIHPNFILESYVNDIALFHLKKAVRYN 181 SDPLMWTAVIGTNNIHGRYPHTKKIKIKAIIIHPNFILESYVNDIALFHLKKAVRYN

Sbjct: 156 ---SDPLMWTAVIGTINIHGEYPHTKKIKIKATITHPNFILESYVNDIALFHLKKAVRYN 326

Query: 182 DYIQPICLPFDVFQILDGNTKCFISGWGRTKEE 214 DYIQPICLPFDVFQILDGNTKCFISGWGRTKEE

Sbjct: 327 DYIQPICLPFDVFQILDGNTECFISGWGRTKEE 427

Identities = 131/131 (100%), Positives = 131/131 (100%) Frame = +3

Query: 215 GNATNILQDAEVHYISREMCHSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP 274 GNATNILQDAEVHYISREMCHSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP

Sbjet: 900 GHATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCEGDSGGPLMCYLP 1079

Query: 275 EYKRFFVMGITSYGHGCGREGFPGVYIGPSFYQEWLTEHFFHASTQGILTINILEGQILI 334 EYERFFVMGITSYGHGCGERGFPGVYIGPSFYQEWLTEHFFHASTQGILTINILEGQILI

Sbjct: 1080 EYKRFFVMGITSYGHGCGREGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILEGQILI 1259

Query: 335 ALCFVILLATT 345 ALCFVILLATT

Shict: 1260 ALCEVILLATT 1292

Identities = 141/153 (92%), Positives = 141/153 (92%) Frame = +3

Query: 62 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVVSLQIKYGRVLVHVCGGTLVRERWVLTAAHC 121 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVVSLQIKYGRVLVHVCGGTLVRE

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Query: 122 TKDSDPLMWTAVIGTNNIHGRYPHTKKIKIKAIIIHPNFILESYVNDIALFHLKKAVRYN 181 SDPLMWTAVIGTNNIHGRYPHTKKIKIKAIIIHPNFILESYVNDIALFHLKKAVRYN

Sbjct: 156 ---SDPLMWTAVIGTNNIHGEYPHTKKIKIKAILIHPNFILESYVNDIALFHLKKAVEYN 326

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Sbjct: 1260 ALCFVILLATT 1292